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Listing of Claims:

1. (currently amended) A method for identifying a potentially transcribed region of interest of a genome comprising:
 - a) Hybridizing a plurality of nucleic acid probes with a nucleic acid sample, wherein said nucleic acid sample comprises transcripts from said genome, wherein said probes are targeting an area of said genome; and
 - b) Identifying said transcribed region as a region of said genome where hybridization of all consecutive probes targeting said region are above a threshold value.
2. (original) The method of Claim 1 wherein said probes are oligonucleotides.
3. (original) The method of Claim 2 wherein said oligonucleotides are immobilized on a substrate.
4. (original) The method of Claim 1 wherein said threshold value is non-specific binding.
5. (original) The method of Claim 4 wherein said non-specific binding is measured using a probe designed to contain at least one mismatched base.
6. (original) The method of Claim 1 further comprising identifying a sub-region wherein hybridization of said probes targeting said sub-regions is similar and indicating said sub-region as said transcribed region.
7. (original) The method of Claim 6 wherein said genome is from a prokaryote.
8. (original) The method of Claim 7 wherein said transcribed region is an operon.
9. (original) The method of Claim 8 wherein said prokaryote is bacteria.
- 10 - 14 (Cancelled)